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RAW SEQUENCE LISTING

DATE: 06/19/2001

PATENT APPLICATION: US/09/748,739

TIME: 12:26:00

Input Set : A:\Ix4143.txt

Output Set: N:\CRF3\06192001\I748739.raw

ENTERED

4 <110> APPLICANT: Lockridge, Oksana
 5 Watkins, Jeffry D.
 7 <120> TITLE OF INVENTION: Butyrylcholinesterase Variants and
 8 Methods of Use
 10 <130> FILE REFERENCE: P-IX 4143
 12 <140> CURRENT APPLICATION NUMBER: US 09/748,739
 C--> 13 <141> CURRENT FILING DATE: 2001-06-01
 15 <160> NUMBER OF SEQ ID NOS: 24
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1967
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Human Butyrylcholinesterase variant
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (86)...(1891)
 30 <400> SEQUENCE: 1
 31 ttaatacgcac tcactatagg gagaccggaa gcttaaggtg cacggccac gtggatcgat 60
 32 cgcgcgacaga tcttcggaag ccacc atg gat agc aaa gtc aca atc ata tgc 112
 33 Met Asp Ser Lys Val Thr Ile Ile Cys
 34 1 5
 36 atc aga ttt ctc ttt tgg ttt ctt ttg ctc tgc atg att ggg aag 160
 37 Ile Arg Phe Leu Phe Trp Phe Leu Leu Cys Met Leu Ile Gly Lys
 38 10 15 20 25
 40 tca cat act gaa gat gac atc ata att gca aca aag aat gga aaa gtc 208
 41 Ser His Thr Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val
 42 30 35 40
 44 aga ggg atg aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt 256
 45 Arg Gly Met Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu
 46 45 50 55
 48 gga att ccc tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag 304
 49 Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys
 50 60 65 70
 52 cca cag tct ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat 352
 53 Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr
 54 75 80 85
 56 gca aat tct tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat 400
 57 Ala Asn Ser Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His
 58 90 95 100 105
 60 gga tca gag atg tgg aac cca aac act gac ctc agt gaa gac tgt tta 448
 61 Gly Ser Glu Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu
 62 110 115 120
 64 tat cta aat gta tgg att cca gca cct aaa cca aaa aat gcc act gta 496
 65 Tyr Leu Asn Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val
 66 125 130 135
 68 ttg ata tgg att tat ggt ggt ggt ttt caa act gga aca tca tct tta 544

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69 Leu Ile Trp Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu
70      140      145      150
72 cat gtt tat gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta 592
73 His Val Tyr Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val
74      155      160      165
76 gtg tca atg aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca 640
77 Val Ser Met Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro
78 170      175      180      185
80 gga aat cct gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg 688
81 Gly Asn Pro Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu
82      190      195      200
84 gct ctt cag tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct 736
85 Ala Leu Gln Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro
86      205      210      215
88 aaa agt gta act ctc ttt gga gaa agt gca gga gca gct tca gtt agc 784
89 Lys Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser
90      220      225      230
92 ctg cat ttg ctt tct cct gga agc cat tca ttg ttc acc aga gcc att 832
93 Leu His Leu Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile
94      235      240      245
96 ctg caa agt ggt tcc ttt aat gct cct tgg gcg gta aca tct ctt tat 880
97 Leu Gln Ser Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr
98 250      255      260      265
100 gaa gct agg aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct 928
101 Glu Ala Arg Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser
102      270      275      280
104 aga gag aat gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc 976
105 Arg Glu Asn Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro
106      285      290      295
108 caa gaa att ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct 1024
109 Gln Glu Ile Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro
110      300      305      310
112 ttg tca gta aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac 1072
113 Leu Ser Val Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp
114      315      320      325
116 atg cca gac ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att 1120
117 Met Pro Asp Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile
118 330      335      340      345
120 ttg gtg ggt gtt aat aaa gat gaa ggg aca tgg ttt tta gtc tat ggt 1168
121 Leu Val Gly Val Asn Lys Asp Glu Gly Thr Trp Phe Leu Val Tyr Gly
122      350      355      360
124 gct cct ggc ttc agc aaa gat aac aat agt atc ata act aga aaa gaa 1216
125 Ala Pro Gly Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu
126      365      370      375
128 ttt cag gaa ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga 1264
129 Phe Gln Glu Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly
130      380      385      390
132 aag gaa tcc atc ctt ttt cat tac aca gac tgg gta gat gat cag aga 1312
133 Lys Glu Ser Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg

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134      395      400      405
136 cct gaa aac tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat 1360
137 Pro Glu Asn Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn
138 410      415      420      425
140 ttc ata tgc cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga 1408
141 Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly
142      430      435      440
144 aat aat gcc ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg 1456
145 Asn Asn Ala Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro
146      445      450      455
148 tgg cca gaa tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc 1504
149 Trp Pro Glu Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val
150      460      465      470
152 ttt ggt tta cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa 1552
153 Phe Gly Leu Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu
154      475      480      485
156 att ttg agt aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat 1600
157 Ile Leu Ser Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr
158 490      495      500      505
160 ggg aat cca aat gag act cag aac aat agc aca agc tgg cct gtc ttc 1648
161 Gly Asn Pro Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe
162      510      515      520
164 aaa agc act gaa caa aaa tat cta acc ttg aat aca gag tca aca aga 1696
165 Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg
166      525      530      535
168 ata atg acg aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt 1744
169 Ile Met Thr Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe
170      540      545      550
172 ttt cca aaa gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg 1792
173 Phe Pro Lys Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp
174      555      560      565
176 gag tgg aaa gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg 1840
177 Glu Trp Lys Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp
178 570      575      580      585
180 aaa aat caa ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt 1888
181 Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly
182      590      595      600
184 ctc taattaatag atctgtcatg atgatcattg caattggatc catatatagg 1941
185 Leu
188 gccctattct atagtgtcac ctaaatt 1967
190 <210> SEQ ID NO: 2
191 <211> LENGTH: 602
192 <212> TYPE: PRT
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Human Butyrylcholinesterase variant
198 <400> SEQUENCE: 2
199 Met Asp Ser Lys Val Thr Ile Ile Cys Ile Arg Phe Leu Phe Trp Phe
200 1      5      10      15

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201 Leu Leu Leu Cys Met Leu Ile Gly Lys Ser His Thr Glu Asp Asp Ile
202          20          25          30
203 Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val
204          35          40          45
205 Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro
206          50          55          60
207 Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp
208 65          70          75          80
209 Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln Asn
210          85          90          95
211 Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn Pro
212          100          105          110
213 Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro
214          115          120          125
215 Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly
216          130          135          140
217 Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe
218 145          150          155          160
219 Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met Asn Tyr Arg Val
220          165          170          175
221 Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu Ala Pro Gly
222          180          185          190
223 Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp Val Gln Lys
224          195          200          205
225 Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu Phe Gly
226          210          215          220
227 Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser Pro Gly
228 225          230          235          240
229 Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe Asn
230          245          250          255
231 Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn Arg Thr Leu
232          260          265          270
233 Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile
234          275          280          285
235 Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu Leu Asn Glu
236          290          295          300
237 Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val Asn Phe Gly Pro
238 305          310          315          320
239 Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp Ile Leu Leu Glu
240          325          330          335
241 Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp
242          340          345          350
243 Glu Gly Thr Trp Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp
244          355          360          365
245 Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile
246          370          375          380
247 Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His
248 385          390          395          400
249 Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala

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250          405          410          415
251 Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu
252          420          425          430
253 Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr
254          435          440          445
255 Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val
256          450          455          460
257 Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg
258 465          470          475          480
259 Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val
260          485          490          495
261 Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln
262          500          505          510
263 Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr
264          515          520          525
265 Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala
266          530          535          540
267 Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met
268 545          550          555          560
269 Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His
270          565          570          575
271 Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr
272          580          585          590
273 Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
274          595          600
277 <210> SEQ ID NO: 3
278 <211> LENGTH: 2416
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Human Butyrylcholinesterase variant
285 <221> NAME/KEY: CDS
286 <222> LOCATION: (214)...(1935)
288 <400> SEQUENCE: 3
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290 ccgaagtatt acatgatttt cactccttgc aaactttacc atctttgttg cagagaatcg 120
291 gaaatcaata tgcatagcaa agtcacaatc atatgcatca gatttctctt ttggtttctt 180
292 ttgctctgca tgcttatttg gaagtcacat act gaa gat gac atc ata att gca 234
293          Glu Asp Asp Ile Ile Ile Ala
294          1          5
296 aca aag aat gga aaa gtc aga ggg atg aac ttg aca gtt ttt ggt ggc 282
297 Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val Phe Gly Gly
298          10          15          20
300 acg gta aca gcc ttt ctt gga att ccc tat gca cag cca cct ctt ggt 330
301 Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
302          25          30          35
304 aga ctt cga ttc aaa aag cca cag tct ctg acc aag tgg tct gat att 378
305 Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile
306 40          45          50          55

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VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date